

**Amendments to the Specification:**

Please delete the current sequence listing and insert the substitute sequence listing after the Abstract.

Please replace the paragraph at page 19, line 37 with the following:

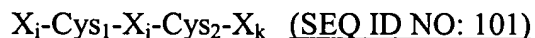
According to preferred aspects of the present invention the compound is a cyclic peptide or analog thereof. Preferably, the compound has the following formula:



wherein  $X_i$  is absent or is a peptide of between 1 and 100 amino acids, preferably between about 1 and 50 amino acids, and more preferably between about 1 and 10;  $X_j$  is 5 amino acids and  $X_k$  is absent or a peptide of between 1 and 100 amino acids, preferably between about 1 and 50 amino acids and more preferably between about 1 and 10, so long as the cyclic peptide or analog thereof retains the qualitative biological activity described above.

Please replace the paragraph at page 21, line 5 with the following:

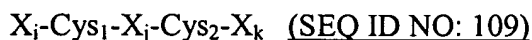
Preferred peptides of the present invention have the following formula:



wherein  $X_i$  is absent or is between 1 and 100 amino acids;  $X_j$  is 5 amino acids and  $X_k$  is absent or between 1 and 100 amino acids. Preferably,  $X_i$  and  $X_k$  are between 1 and 50 amino acids and more preferably between 1 and 10 amino acids.

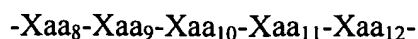
Please replace the paragraph at page 21, line 10 with the following:

By way of exemplification and not limitation, ~~preferred~~ preferred peptides of the present invention include the peptides described in Figure 4. In general, a preferred peptide has the formula:



wherein;

$X_j$  has the formula



and  $Xaa_8$  is an amino acid selected from the group ~~consisting~~ consisting of Trp, Thr, Ala, Phe, Leu, Met and Tyr;  $Xaa_9$  is an amino acid selected from the group consisting of Thr, Asp and Ala;

Xaa<sub>10</sub> is an amino acid selected from the group consisting of Trp, Ala, Phe, Leu and Tyr; Xaa<sub>11</sub> is an amino acid selected from the group consisting of Glu, Ala, Arg and Gln; and Xaa<sub>12</sub> is an amino acid selected from the group consisting of Gly, Asp, Thr, Ser and Ala.

Please replace the paragraph at page 21, lines 23 with the following:

As a further example, preferred peptides have the formula:

Xaa<sub>1</sub>- Xaa<sub>2</sub>- Xaa<sub>3</sub>- Xaa<sub>4</sub>- Xaa<sub>5</sub>- Xaa<sub>6</sub>-Cys- Xaa<sub>8</sub>- Xaa<sub>9</sub>- Xaa<sub>10</sub>- Xaa[[1]]<sub>11</sub>- Xaa[[1]]<sub>12</sub>-Cys- Xaa<sub>14</sub>- Xaa<sub>15</sub>- Xaa<sub>16</sub>- Xaa<sub>17</sub>- Xaa<sub>18</sub> (SEQ ID NO: 102)

wherein Xaa<sub>1</sub> is any amino acid; Xaa<sub>2</sub> is any amino acid; Xaa<sub>3</sub> is an amino acid selected from the group consisting of Trp, Phe, Leu, Ala, Met and Val; Xaa<sub>4</sub> is an amino acid; Xaa<sub>5</sub> is an amino acid selected from the group consisting of Val, Ile, Ala, Trp and Tyr; Xaa<sub>6</sub> is an amino acid selected from the group consisting of Leu, Ile, Met, Val and Ala; Xaa<sub>8</sub> is selected from the group consisting of Trp, Phe, Leu, Met, Ala and Val; Xaa<sub>9</sub> is an amino acid; Xaa<sub>10</sub> is an amino acid selected from the group consisting of Trp, Phe, Met and Tyr; Xaa<sub>11</sub> is any amino acid; Xaa<sub>12</sub> is any amino acid; Xaa<sub>14</sub> is any amino acid except Pro; Xaa<sub>15</sub> is an amino acid selected from the group consisting of Arg, Lys, Leu, Trp, His and Met; Xaa<sub>16</sub> is any amino acid; Xaa<sub>17</sub> is any amino acid; and Xaa<sub>18</sub> is any amino acid.

Please replace the paragraph at page 40, line 38 with the following:

*Phage Libraries* - The random sequence polyvalent peptide phage libraries have been described previously (Lowman, H. B., *et al.*, *Biochemistry* 37:8870 (1998)). The peptide libraries were of the form X<sub>i</sub>CX<sub>j</sub>CX<sub>k</sub> (SEQ ID NO:103) (where X was any of the 20 naturally occurring L-amino acids and j ranged from 4-10 and i + j + k=18), an unconstrained library X<sub>20</sub> (SEQ ID NO:104), and X<sub>4</sub>CX<sub>2</sub>GPX<sub>4</sub>CX<sub>4</sub> (SEQ ID NO:105). Each of the 10 libraries has in excess of 10<sup>8</sup> clones.

Please replace the paragraph at page 41, line 1 with the following:

*Selection Conditions* - TF<sub>1-243</sub> (Paborsky, L. R., *et al.*, *J. Biol. Chem.* 266: 21911 (1991)) or recombinant human FVIIa (2 µg/ml each) were immobilized directly to ~~Maxisorp~~ MaxiSorp™ plates (Nunc) in 50 mM ammonium bicarbonate, pH 9.3 by incubating overnight at 4 °C. Wells were blocked using Sorting Buffer (50 mM HEPES, pH 7.2, 5 mM CaCl<sub>2</sub>, 5 mM MgCl<sub>2</sub>, 150 mM NaCl, 1% BSA) for 1 h at 25 °C. Recombinant human FVIIa (2 µg/ml) in Sorting Buffer

was added for 30 min to wells previously coated and blocked with TF to form the TF-FVIIa complex. Phage from the libraries described above were pooled into 3 groups. Pool A contained  $X_iCX_jCX_k$  (SEQ ID NO:103) where  $j = 5 - 7$ ; Pool B contained  $X_4CX_2GPX_4CX_4$  (SEQ ID NO:105),  $X_{20}$  (SEQ ID NO:104) and  $X_iCX_jCX_k$  (SEQ ID NO:103) where  $j = 4$ ; Pool E contained  $X_iCX_jCX_k$  (SEQ ID NO:103) where  $j = 8 - 10$ . Phage from each pool were incubated with the immobilized targets in Sorting Buffer for 3 h at 25 °C.; generally about  $5 \times 10^{10}$  phage were added at the beginning of each round. Unbound phage were removed by repetitive washing with Wash Buffer (50 mM HEPES, pH 7.2, 150 mM NaCl, 0.005% Tween 20<sup>TM</sup>); remaining phage were eluted with 500 mM KCl, 10 mM HCl, pH 2. The eluted phage were then propagated in XL1-Blue cells with VCSM13 helper phage (Stratagene<sup>TM</sup>) overnight at 37 °C. Enrichment could be monitored by titering the number of phage which bound to a target coated well compare to a well coated with BSA.

Please replace Table II at page 48 with the following:

Table II. Sequences Selected Using Selected Full Randomization of the A Series

SEQUENCE ID. NO.	CLONE	DEDUCED AMINO ACID SEQUENCE																			
<u>106</u>	Library AoN	o	o	X	W	E	V	X	C	W	X	W	E	X	C	X	X	X	X	X	X
76	AN41			A	W	E	V	L	C	W	A	W	E	D	C	E	R	G	A	G	S
77	AN33			A	W	E	V	V	C	W	S	W	E	T	C	E	R	G	E	T	P
78	AN31			E	W	E	V	V	C	W	A	W	E	T	C	E	R	G	E	R	Q
79	AN43			E	W	E	V	L	C	W	E	W	E	V	C	E	R	D	I	T	L
80	AN42			E	W	E	V	V	C	W	T	W	E	A	C	E	L	G	E	R	V
81	AN32			G	W	E	V	V	C	W	S	W	E	S	C	A	R	G	D	L	E
<u>107</u>	Library AoNC	o	o	X	W	E	V	X	C	W	X	W	E	X	C	X	o	o	o	o	o
82	ANC45			A	W	E	V	V	C	W	S	W	E	T	C	E					
83	ANC41			E	W	E	V	V	C	W	E	W	E	N	C	L					
84	ANC33			E	W	E	V	L	C	W	G	W	E	T	C	S					
85	ANC34			G	W	E	V	L	C	W	T	W	E	E	C	S					

86	ANC43	S	W	E	V	L	C	W	Q	W	E	E	C	E						
87	ANC32	T	W	E	V	L	C	W	S	W	E	S	C	E						
<u>108</u>	Library A	X	X	X	W	E	V	X	C	W	X	W	E	X	C	X	X	X	X	X
88	AP31	M	E	T	W	E	V	L	C	W	E	W	E	E	C	V	R	G	G	E
89	AP32	A	V	E	W	E	V	I	C	W	A	W	E	T	C	E	R	S	N	M
90	AP33	A	V	Q	W	E	V	L	C	W	Q	W	E	N	C	H	R	G	E	Q
91	AP34	M	Q	G	W	E	V	V	C	W	E	W	E	G	C	A	R	G	D	H
92	AP42	E	E	Q	W	E	V	V	C	W	D	W	E	T	C	D	W	P	G	K
93	AP43	L	G	E	W	E	V	M	C	W	T	W	E	S	C	G	W	P	V	G
94	AP44	M	L	D	W	E	V	V	C	W	T	W	E	S	C	V	R	E	G	K
95	AP45	K	N	G	W	E	V	L	C	W	T	W	E	T	C	G	R	G	V	G
96	AP35	G	A	P	W	E	V	V	C	W	S	W	E	S	C	S	W	G	V	A
97	AP41	E	D	L	W	E	V	V	C	W	S	W	E	A	C	S	R	E	G	T

- Peptide sequences were deduced from the DNA sequence of clones obtained after 4 rounds of selection.
- Shaded residues indicate the wildtype sequence which was fixed; underlined residues were fully randomized as described in text.
- "o" indicates no amino acid.